

STIC-Biotech/ChemLib

196715

From: Bausch, Sarae  
Sent: Wednesday, July 26, 2006 5:37 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 10/663497

Please do a standard nucleic acid sequence search encoding the amino acid sequence of SEQ ID No. 25, residues 158-163, for 10/663497. Please print out the first 50 hits.

Thank you.

Sarac Bausch, Ph.D.  
USPTO Art Unit 1634  
REM 2 A 70  
Mailbox: REM 2 C 70  
(571) 272-2912

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 1, 2006, 10:35:50 ; Search time 2272 Seconds

(without alignments)  
221.511 Million cell updates/sec

Title: US-10-663-497A-25\_COPY\_158\_163

Perfect score: 31

Sequence: 1 MTTVP 6

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q-/abs/ABSWEB\_spool/US10663497/runat\_01082006\_083600\_1288/app\_query.fasta\_1  
-DB=EST -Qfmt=fastap -SUPPLX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi -LIST=150  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes06h  
-USER=US10663497 @CN 1 1 4769 @runat\_01082006\_083600\_1288 -NCPU=6 -ICPU=3  
-NO\_MAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPEXT=7  
-FGAPOPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb\_est6:\*

6: gb\_hic:\*

7: gb\_est2:\*

8: gb\_est7:\*

9: gb\_est8:\*

10: gb\_est9:\*

11: gb\_ges1:\*

12: gb\_ges2:\*

13: gb\_ges3:\*

14: gb\_ges4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match | Length | ID       | Description |
|--------|-----|-------|-------------|--------|----------|-------------|
| 1      | 31  | 100.0 | 180         | 1      | AJ463628 | AJ463628    |
| 2      | 31  | 100.0 | 217         | 7      | BB112240 | BB112240    |
| 3      | 31  | 100.0 | 223         | 13     | CL221902 | CL221902    |
| 4      | 31  | 100.0 | 230         | 7      | BB063656 | BB063656    |

|          |             |
|----------|-------------|
| BF900869 | IL2-MT017   |
| AV282051 | AV282051    |
| AV142411 | AV142411    |
| AV330138 | AV330138    |
| CZ259261 | BC071138    |
| CV831343 | IDOACC18A   |
| BB420250 | BB420250    |
| BB720743 | BB720743    |
| AI650253 | wa17f06.x   |
| CK880041 | SGP140332   |
| BB455432 | BA455432    |
| BB194369 | BB194369    |
| BB407564 | BB407564    |
| CX263247 | LB1645.cd   |
| BB386771 | BB386771    |
| CD872467 | AZ02.120K   |
| BB192244 | BB192244    |
| BB405411 | BB405411    |
| BB432442 | BB432442    |
| BB339341 | BB339341    |
| BB375154 | BB375154    |
| BB123949 | BB123949    |
| BB137719 | BB137719    |
| BB463421 | BB463421    |
| BB122366 | BB122366    |
| DY218704 | 000219BOV   |
| BB257508 | BB257508    |
| BB367725 | BB367725    |
| W36164   | 213 Mouse V |
| AW604092 | IL3-CT021   |
| BH610392 | SALK_0088   |
| BY123236 | BY123236    |
| BY103137 | BY103137    |
| BB131656 | BB131656    |
| BB207693 | BB207693    |
| BB249936 | BB249936    |
| CL366355 | RPC144_35   |
| BY304673 | BY304673    |
| CG512001 | OST64704    |
| CL3316   | YuJ1        |
| CG086613 | PUBB390TB   |
| CV428815 | EST02044    |
| AW308438 | 3736 MARC   |
| CE293776 | tigr-g88-   |
| BE624513 | uu23a10.y   |
| D69147   | CELK06504F  |
| BG629299 | CC-88f1CL   |
| BE688274 | uw59D06.y   |
| CG495711 | OST35264    |
| CG611802 | OST297239   |
| AV766938 | AV766938    |
| CN470928 | hh.Ab.Bra   |
| CG500417 | OST43241    |
| AI504289 | v103e01.x   |
| CG508897 | OST59710    |
| AV202038 | AV202038    |
| BQ499068 | EST08293    |
| CG577010 | EST212338   |
| AA752646 | 96SU0139    |
| CG503960 | OST51453    |
| AI117812 | uc40d10.i   |
| AA250694 | mx85b05.f   |
| W53543   | md56a04.r1  |
| CG631195 | OST352592   |
| AA031074 | ml48R01.i   |
| BY105532 | BY105532    |
| CG503954 | OST51432    |
| AL397575 | T7 end of   |
| CG545882 | OST144637   |
| CG612943 | OST299598   |
| CG42888  | OST379822   |
| CG508603 | OST59268    |
| CG576780 | OST211879   |

|     |    |       |     |    |          |                   |
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| 78  | 31 | 100.0 | 403 | 12 | CG596058 | OST257279         |
| 79  | 31 | 100.0 | 403 | 12 | CG671065 | OST472406         |
| 80  | 31 | 100.0 | 404 | 12 | CG511362 | OST63584          |
| 81  | 31 | 100.0 | 404 | 12 | CG610121 | OST292460         |
| 82  | 31 | 100.0 | 405 | 12 | CG055853 | SALK_0977         |
| 83  | 31 | 100.0 | 405 | 12 | CG508250 | OST58762          |
| 84  | 31 | 100.0 | 405 | 12 | CG512427 | OST65358          |
| 85  | 31 | 100.0 | 406 | 11 | BH014919 | TDCBSA6TH         |
| 86  | 31 | 100.0 | 408 | 4  | BY093847 | BY093847          |
| 87  | 31 | 100.0 | 410 | 1  | AA268982 | va99d06.r         |
| 88  | 31 | 100.0 | 411 | 4  | BY288280 | BY288280          |
| 89  | 31 | 100.0 | 414 | 4  | BX515944 | BX515944          |
| 90  | 31 | 100.0 | 419 | 7  | AW479331 | 24715 MAR         |
| 91  | 31 | 100.0 | 421 | 3  | BO980023 | OGG18B18          |
| 92  | 31 | 100.0 | 422 | 7  | BE855107 | BE855107          |
| 93  | 31 | 100.0 | 422 | 12 | CU192004 | 104 414 1         |
| 94  | 31 | 100.0 | 423 | 11 | AQ640114 | 927P1-2D1         |
| 95  | 31 | 100.0 | 424 | 7  | BE600010 | P11 78 DO         |
| 96  | 31 | 100.0 | 425 | 1  | AA524192 | AA524192 ng3609.s |
| 97  | 31 | 100.0 | 432 | 7  | AW287335 | LGI 269 F         |
| 98  | 31 | 100.0 | 439 | 14 | AG255606 | Lotus Cor         |
| 99  | 31 | 100.0 | 452 | 7  | BF195890 | 7087a02.x         |
| 100 | 31 | 100.0 | 453 | 1  | A1144965 | UI-R-BT0          |
| 101 | 31 | 100.0 | 463 | 8  | CV834432 | IDOACC25C         |
| 102 | 31 | 100.0 | 453 | 8  | CV837522 | IDOACC5BF         |
| 103 | 31 | 100.0 | 453 | 10 | DV421484 | NADY570TR         |
| 104 | 31 | 100.0 | 459 | 7  | BE197227 | ug7b01.y          |
| 105 | 31 | 100.0 | 459 | 7  | BE627359 | uc87f02.x         |
| 106 | 31 | 100.0 | 461 | 1  | AA855845 | vw75f02.r         |
| 107 | 31 | 100.0 | 465 | 4  | CB715119 | AMGNUG:N          |
| 108 | 31 | 100.0 | 466 | 7  | BE448145 | ut80b03.y         |
| 109 | 31 | 100.0 | 466 | 7  | BE597646 | P11 72 DO         |
| 110 | 31 | 100.0 | 468 | 1  | AA194371 | zq05c03.s         |
| 111 | 31 | 100.0 | 468 | 9  | DA302156 | DA302156          |
| 112 | 31 | 100.0 | 469 | 7  | BE400108 | AWB011.B0         |
| 113 | 31 | 100.0 | 470 | 7  | BE448495 | ut90f01.y         |
| 114 | 31 | 100.0 | 470 | 7  | BE599215 | P11 86 G0         |
| 115 | 31 | 100.0 | 474 | 7  | BE650827 | UI-M-BH3          |
| 116 | 31 | 100.0 | 477 | 7  | BE653213 | UI-M-ANO          |
| 117 | 31 | 100.0 | 481 | 7  | AW489629 | UI-M-BH3          |
| 118 | 31 | 100.0 | 481 | 7  | AW493902 | UI-M-BH3          |
| 119 | 31 | 100.0 | 482 | 2  | B1173984 | OSTF009H5         |
| 120 | 31 | 100.0 | 491 | 1  | AA690651 | vu35e10.r         |
| 121 | 31 | 100.0 | 497 | 4  | BX511885 | BX511885          |
| 122 | 31 | 100.0 | 500 | 5  | CD599903 | CD599903          |
| 123 | 31 | 100.0 | 503 | 1  | AA386922 | vc23d12.r         |
| 124 | 31 | 100.0 | 505 | 7  | AW624748 | EST122693         |
| 125 | 31 | 100.0 | 507 | 4  | CA249653 | SCRUF111          |
| 126 | 31 | 100.0 | 511 | 7  | AW944928 | EST336978         |
| 127 | 31 | 100.0 | 512 | 7  | AW490025 | UI-M-BH3          |
| 128 | 31 | 100.0 | 514 | 10 | DV552243 | 122000b11         |
| 129 | 31 | 100.0 | 517 | 7  | BE595457 | P11 55 G0         |
| 130 | 31 | 100.0 | 517 | 7  | B1927198 | EST547087         |
| 131 | 31 | 100.0 | 519 | 7  | BB867484 | BB867484          |
| 132 | 31 | 100.0 | 519 | 7  | BE599938 | P11 77 E1         |
| 133 | 31 | 100.0 | 519 | 10 | DT177202 | JGI ANO4          |
| 134 | 31 | 100.0 | 520 | 1  | AU249853 | AU249853          |
| 135 | 31 | 100.0 | 520 | 11 | AZ132104 | OSUNB005          |
| 136 | 31 | 100.0 | 521 | 7  | BF470230 | UI-M-BH3          |
| 137 | 31 | 100.0 | 522 | 7  | BE596226 | P11 51 B0         |
| 138 | 31 | 100.0 | 524 | 4  | BX525148 | BX525148          |
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| 140 | 31 | 100.0 | 526 | 4  | CB438008 | 685913 MA         |
| 141 | 31 | 100.0 | 527 | 2  | B1211968 | IP1 62 G0         |
| 142 | 31 | 100.0 | 533 | 2  | BF923102 | QV4-NT025         |
| 143 | 31 | 100.0 | 534 | 9  | DB351716 | DB351716          |
| 144 | 31 | 100.0 | 534 | 12 | CG680080 | ZWMB0032          |
| 145 | 31 | 100.0 | 537 | 12 | BZ635050 | OCB105TM          |
| 146 | 31 | 100.0 | 538 | 11 | BH015137 | TGGBV42TH         |
| 147 | 31 | 100.0 | 540 | 4  | BX557881 | BX557881          |
| 148 | 31 | 100.0 | 544 | 8  | CN185253 | UCRC05 0          |
| 149 | 31 | 100.0 | 545 | 1  | AJ407475 | AJ407475          |
| 150 | 31 | 100.0 | 545 | 11 | AZ254990 | RPCI-23-1         |

ALIGNMENTS

RESULT 1

AJ463628

LOCUS

DEFINITION

180 bp mRNA linear EST 24-MAY-2002

subsp. vulgare cDNA clone

ACCSSION

AJ463628

VERSION

GI:21062548

KEYWORDS

EST

SOURCE

Hordeum vulgare subsp. vulgare

ORGANISM

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Poideae; Triticeae; Hordeum.

REFERENCE

1 (bases 1 to 180)

AUTHORS

Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.

TITLE

Barley EST's

JOURNAL

Unpublished (2002)

COMMENT

Institute of Biotechnology  
University of Helsinki  
P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014, Finland.

FEATURES

Location/Qualifiers

1..180

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Saana"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="S000020007F10F1"

/dev\_stage="Embryo"

/clone\_lib="S00002"

/note="1 day after pollination"

ORIGIN

Alignment Scores:

Pred. No.:

3.02e+03

Length:

180

Score:

31.00

Matches:

6

Percent Similarity:

100.0%

Conservative:

0

Best Local Similarity:

100.0%

Mismatches:

0

Query Match:

100.0%

Indels:

0

DB:

1

Gaps:

0

US-10-663-497A-25\_COPY\_158\_163 (1-6) x AJ463628 (1-180)

Qy

1 MetThrThrThrValPro 6

Db

33 ATGACGACAACTGTACCA 50

RESULT 2

BH112240

LOCUS

DEFINITION

217 bp mRNA linear EST 27-JUN-2000

musculus cDNA clone 9530034K15 3', mRNA sequence.

ACCSSION

BH112240

VERSION

GI:8764808

KEYWORDS

EST

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 217)

AUTHORS

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Iwawa,M., Kadoya,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 1, 2006, 10:23:46 ; Search time 418 Seconds  
(without alignments)  
150.120 Million cell updates/sec

Title: US-10-663-497A-25\_COPY\_158\_163

Perfect score: 31

Sequence: 1 MTTVP 6

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abse/ABSSWEB\_spool/US1063497/runat\_01082006\_083556\_1248/app\_query.fasta.1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h  
-USER=US1063497 @CGM\_1\_1761 @runat\_01082006\_083556\_1248 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq\_8.\*

1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 31    | 100.0       | 18     | 14 | ADY98104    |
| 2          | 31    | 100.0       | 25     | 9  | ACH65851    |
| 3          | 31    | 100.0       | 39     | 12 | ADL64531    |

|    |    |       |        |    |          |
|----|----|-------|--------|----|----------|
| 4  | 31 | 100.0 | 153    | 13 | ADS01729 |
| 5  | 31 | 100.0 | 420    | 6  | ABN92824 |
| 6  | 31 | 100.0 | 420    | 13 | ADS02980 |
| 7  | 31 | 100.0 | 430    | 6  | ABN87768 |
| 8  | 31 | 100.0 | 453    | 10 | ADB51509 |
| 9  | 31 | 100.0 | 496    | 14 | ADY98093 |
| 10 | 31 | 100.0 | 499    | 14 | ADY98092 |
| 11 | 31 | 100.0 | 509    | 4  | AAH88202 |
| 12 | 31 | 100.0 | 554    | 13 | ACN46715 |
| 13 | 31 | 100.0 | 648    | 13 | ADR59534 |
| 14 | 31 | 100.0 | 784    | 10 | ADC30255 |
| 15 | 31 | 100.0 | 804    | 14 | AEC32074 |
| 16 | 31 | 100.0 | 906    | 4  | AAH53216 |
| 17 | 31 | 100.0 | 930    | 8  | ABZ52453 |
| 18 | 31 | 100.0 | 1059   | 6  | ABZ14283 |
| 19 | 31 | 100.0 | 1059   | 8  | ADA68644 |
| 20 | 31 | 100.0 | 1095   | 10 | ABZ68336 |
| 21 | 31 | 100.0 | 1095   | 14 | ADY98080 |
| 22 | 31 | 100.0 | 1095   | 14 | AED60524 |
| 23 | 31 | 100.0 | 1098   | 10 | ABZ68334 |
| 24 | 31 | 100.0 | 1098   | 14 | ADY98076 |
| 25 | 31 | 100.0 | 1098   | 14 | AED60520 |
| 26 | 31 | 100.0 | 1113   | 11 | ACL33708 |
| 27 | 31 | 100.0 | 1274   | 14 | ACL72110 |
| 28 | 31 | 100.0 | 1319   | 2  | AAH06841 |
| 29 | 31 | 100.0 | 1336   | 3  | AAH47532 |
| 30 | 31 | 100.0 | 1339   | 3  | AAH34681 |
| 31 | 31 | 100.0 | 1448   | 4  | AAH29729 |
| 32 | 31 | 100.0 | 1857   | 12 | ADQ35434 |
| 33 | 31 | 100.0 | 1884   | 13 | ADQ60328 |
| 34 | 31 | 100.0 | 2000   | 11 | ACL34911 |
| 35 | 31 | 100.0 | 3112   | 4  | AAH16200 |
| 36 | 31 | 100.0 | 3150   | 13 | ADQ87365 |
| 37 | 31 | 100.0 | 3259   | 4  | AAH54766 |
| 38 | 31 | 100.0 | 3349   | 4  | AAH54143 |
| 39 | 31 | 100.0 | 3713   | 4  | AAH54416 |
| 40 | 31 | 100.0 | 11382  | 14 | ACL64441 |
| 41 | 31 | 100.0 | 27204  | 11 | ACN44866 |
| 42 | 31 | 100.0 | 37500  | 12 | ADH48029 |
| 43 | 31 | 100.0 | 67212  | 3  | AAA08954 |
| 44 | 31 | 100.0 | 92112  | 13 | ADQ99457 |
| 45 | 31 | 100.0 | 107320 | 11 | ACN44736 |
| 46 | 31 | 100.0 | 118935 | 14 | ADZ13136 |
| 47 | 31 | 100.0 | 123219 | 4  | AAH88703 |
| 48 | 31 | 100.0 | 138627 | 12 | ADQ97183 |
| 49 | 31 | 100.0 | 151830 | 12 | ADH51151 |
| 50 | 31 | 100.0 | 151830 | 12 | ADH78027 |
| 51 | 31 | 100.0 | 151830 | 14 | AEA48114 |
| 52 | 31 | 100.0 | 193789 | 14 | AED89415 |
| 53 | 30 | 96.8  | 21     | 2  | AAH34897 |
| 54 | 30 | 96.8  | 318    | 1  | AAH50343 |
| 55 | 30 | 96.8  | 321    | 14 | AED43896 |
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| 58 | 30 | 96.8  | 455    | 8  | ABZ52892 |
| 59 | 30 | 96.8  | 491    | 6  | ABN24660 |
| 60 | 30 | 96.8  | 642    | 13 | ADS48627 |
| 61 | 30 | 96.8  | 651    | 12 | ADJ42877 |
| 62 | 30 | 96.8  | 793    | 5  | ABA18007 |
| 63 | 30 | 96.8  | 1029   | 8  | ADQ29993 |
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| 65 | 30 | 96.8  | 1308   | 10 | ABX07812 |
| 66 | 30 | 96.8  | 1308   | 12 | ADN92007 |
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| 69 | 30 | 96.8  | 1323   | 14 | AEA57833 |
| 70 | 30 | 96.8  | 1407   | 2  | ACA30774 |
| 71 | 30 | 96.8  | 1436   | 2  | AAV52429 |
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| 73 | 30 | 96.8  | 1609   | 13 | ADM44893 |
| 74 | 30 | 96.8  | 1684   | 13 | ADM47742 |
| 75 | 30 | 96.8  | 1971   | 10 | ADF42467 |
| 76 | 30 | 96.8  | 2065   | 3  | AAC44909 |

|          |                  |
|----------|------------------|
| AGS01729 | Staphyloc        |
| ABN92824 | Staphyloc        |
| ADQ02980 | Staphyloc        |
| ABN87768 | Human pro        |
| ADB51509 | Primary r        |
| ADY98093 | Human TIM        |
| ADY98092 | Human TIM        |
| AH88202  | CNS disor        |
| ACN46715 | Cotton pr        |
| ADR59534 | Cotton cd        |
| ADC30255 | Human nov        |
| AEC32074 | Human CG5        |
| AAH53216 | S. epider        |
| ABZ52453 | Aspergill        |
| ABZ14283 | Arabidops        |
| ADA68644 | Arabidops        |
| ABZ68336 | Nucleotid        |
| ADY98080 | Human TIM        |
| AED60524 | Human TIM        |
| ABZ68334 | Nucleotid        |
| ADY98076 | Human TIM        |
| AED60520 | Human TIM        |
| ACL33708 | Rice abio        |
| ACL72110 | M. xanthu        |
| AAH06841 | Arabidops        |
| AAH47532 | Arabidops        |
| AAH34681 | Arabidops        |
| AH29729  | S cerevis        |
| ADQ35434 | Novel mou        |
| ADQ60328 | Bacterial        |
| ACL34911 | Rice stre        |
| AH16200  | Human CDN        |
| ADQ87365 | Human tum        |
| AAH54766 | S. epider        |
| AAH54143 | S. epider        |
| AAH54416 | S. epider        |
| ACL64441 | M. xanthu        |
| ACN44866 | Human gen        |
| ADH48029 | Clone PS3        |
| AAA08954 | WFS1 vari        |
| ADQ99457 | Continuati (4 of |
| ACN44736 | Mouse gen        |
| ADZ13136 | Murine ca        |
| AAH88703 | Human DNA        |
| ADQ97183 | Human can        |
| ADH51151 | Protein p        |
| ADH78027 | Human PPP        |
| AEA48114 | Human PPP        |
| AED89415 | Human bre        |
| AAH34897 | PCR prime        |
| AAH50343 | DNA encod        |
| AED43896 | Human epi        |
| AAH51681 | Human sec        |
| ACL28553 | Rice abio        |
| ABZ52892 | Aspergill        |
| ABN24660 | Human ORF        |
| ADS48627 | Bacterial        |
| ADJ42877 | Plant tra        |
| ABA18007 | Human ner        |
| ADQ29993 | Plant ful        |
| ACA38856 | Prokaryot        |
| ABX07812 | S. pneumo        |
| ADN92007 | S. pneumo        |
| ADK45553 | Streptoco        |
| ADR93963 | Novel S.         |
| AEA57833 | Streptoco        |
| ACA30774 | Prokaryot        |
| AAV52429 | Streptoco        |
| AAH3842  | C. pneumo        |
| ADM44893 | Bacterial        |
| ADM47742 | Polynucle        |
| ADF42467 | Human PP8        |
| AAC44909 | Arabidops        |

|       |    |      |        |    |              |                    |       |    |      |     |   |          |                    |
|-------|----|------|--------|----|--------------|--------------------|-------|----|------|-----|---|----------|--------------------|
| 77    | 30 | 96.8 | 2130   | 13 | ADT05720     | Adt05720 Haemophil | C 150 | 28 | 90.3 | 207 | 4 | ABS43765 | ABS43765 Human liv |
| 78    | 30 | 96.8 | 2442   | 11 | ACL26871     | ACL26871 Rice abio |       |    |      |     |   |          |                    |
| C 79  | 30 | 96.8 | 2518   | 3  | AZ60655      | Az60655 DNA encod  |       |    |      |     |   |          |                    |
| C 80  | 30 | 96.8 | 2600   | 2  | AAQ90096     | AaQ90096 Mouse kap |       |    |      |     |   |          |                    |
| C 81  | 30 | 96.8 | 2600   | 6  | AAI72372     | AaI72372 KOR3 gene |       |    |      |     |   |          |                    |
| C 82  | 30 | 96.8 | 2600   | 10 | ADD49196     | Add49196 Mouse kap |       |    |      |     |   |          |                    |
| C 83  | 30 | 96.8 | 2634   | 3  | AZ60653      | Az60653 DNA encod  |       |    |      |     |   |          |                    |
| C 84  | 30 | 96.8 | 2742   | 10 | ADH84750     | Adh84750 Enterococ |       |    |      |     |   |          |                    |
| 85    | 30 | 96.8 | 3597   | 13 | ADS7926      | Ads7926 Bacterial  |       |    |      |     |   |          |                    |
| 86    | 30 | 96.8 | 3624   | 10 | ADL13647     | Adl13647 Osteoarth |       |    |      |     |   |          |                    |
| 87    | 30 | 96.8 | 3624   | 10 | ADL13650     | Adl13650 Osteoarth |       |    |      |     |   |          |                    |
| 88    | 30 | 96.8 | 3624   | 13 | ADR46384     | Adr46384 Human epi |       |    |      |     |   |          |                    |
| 89    | 30 | 96.8 | 3624   | 14 | ADV42485     | Adv42485 Human psy |       |    |      |     |   |          |                    |
| 90    | 30 | 96.8 | 3756   | 8  | ACA33339     | Aca33339 Prokaryot |       |    |      |     |   |          |                    |
| 91    | 30 | 96.8 | 4061   | 2  | AAT44518     | Aat44518 Hib hxC   |       |    |      |     |   |          |                    |
| 92    | 30 | 96.8 | 4118   | 2  | AAT44520     | Aat44520 NTHI hxC  |       |    |      |     |   |          |                    |
| 93    | 30 | 96.8 | 4306   | 10 | ABX74461     | Abx74461 Human cDN |       |    |      |     |   |          |                    |
| 94    | 30 | 96.8 | 4400   | 2  | AAV43590     | Aav43590 Human epi |       |    |      |     |   |          |                    |
| 95    | 30 | 96.8 | 4651   | 2  | AAT44519     | Aat44519 NTHI hxC  |       |    |      |     |   |          |                    |
| 96    | 30 | 96.8 | 4868   | 10 | ADL13651     | Adl13651 Osteoarth |       |    |      |     |   |          |                    |
| 97    | 30 | 96.8 | 4871   | 10 | ADL13646     | Adl13646 Osteoarth |       |    |      |     |   |          |                    |
| 98    | 30 | 96.8 | 4871   | 14 | AEB96739     | Aeb96739 Human EGF |       |    |      |     |   |          |                    |
| 99    | 30 | 96.8 | 4871   | 14 | AED18058     | Aed18058 Fibrotic  |       |    |      |     |   |          |                    |
| 100   | 30 | 96.8 | 4877   | 4  | AAH28219     | Aah28219 Nucleotid |       |    |      |     |   |          |                    |
| 101   | 30 | 96.8 | 4877   | 6  | ABV94209     | Abv94209 Breast ca |       |    |      |     |   |          |                    |
| 102   | 30 | 96.8 | 4877   | 13 | ADR5827      | Adr5827 Human pro  |       |    |      |     |   |          |                    |
| 103   | 30 | 96.8 | 4877   | 13 | ADR66511     | Adr66511 Human pro |       |    |      |     |   |          |                    |
| 104   | 30 | 96.8 | 4877   | 13 | ADT93117     | Adt93117 Human epi |       |    |      |     |   |          |                    |
| 105   | 30 | 96.8 | 4877   | 13 | ADP76050     | Adp76050 DNA of hu |       |    |      |     |   |          |                    |
| 106   | 30 | 96.8 | 5007   | 4  | AAK51657     | Aak51657 Human pol |       |    |      |     |   |          |                    |
| 107   | 30 | 96.8 | 5032   | 4  | ABA09190     | Aba09190 Human pre |       |    |      |     |   |          |                    |
| 108   | 30 | 96.8 | 5032   | 4  | AAK52641     | Aak52641 Human pro |       |    |      |     |   |          |                    |
| 109   | 30 | 96.8 | 7814   | 13 | ADT05510     | Adt05510 Haemophil |       |    |      |     |   |          |                    |
| C 110 | 30 | 96.8 | 8372   | 10 | ABX94036     | Abx94036 Rat orpha |       |    |      |     |   |          |                    |
| C 111 | 30 | 96.8 | 8372   | 14 | ABE47223     | Aeb47223 Rat orpha |       |    |      |     |   |          |                    |
| C 112 | 30 | 96.8 | 8372   | 14 | ABE77224     | Aeb77224 Rat orpha |       |    |      |     |   |          |                    |
| 113   | 30 | 96.8 | 16878  | 3  | AAAB1515     | Aaa81515 N. mening |       |    |      |     |   |          |                    |
| 114   | 30 | 96.8 | 19031  | 2  | AAH13104     | Aax13104 Enterococ |       |    |      |     |   |          |                    |
| 115   | 30 | 96.8 | 19031  | 6  | ABS98899     | Abs98899 Enterococ |       |    |      |     |   |          |                    |
| 116   | 30 | 96.8 | 26309  | 4  | AAAS59535    | Aas59535 Propionib |       |    |      |     |   |          |                    |
| C 117 | 30 | 96.8 | 26309  | 8  | ACF64464     | Acf64464 Propionib |       |    |      |     |   |          |                    |
| C 118 | 30 | 96.8 | 31960  | 9  | ACD18998     | Acd18998 E. coli 0 |       |    |      |     |   |          |                    |
| C 119 | 30 | 96.8 | 35910  | 10 | ADC00933     | Adc00933 Enterohae |       |    |      |     |   |          |                    |
| 120   | 30 | 96.8 | 66986  | 4  | AAF28542     | Aaf28542 Genomic f |       |    |      |     |   |          |                    |
| 121   | 30 | 96.8 | 110000 | 2  | AAAT4063_02  | Continuation (3 of |       |    |      |     |   |          |                    |
| C 122 | 30 | 96.8 | 110000 | 2  | AAAX91990_03 | Continuation (4 of |       |    |      |     |   |          |                    |
| C 123 | 30 | 96.8 | 110000 | 3  | AAA81490_09  | Continuation (10 o |       |    |      |     |   |          |                    |
| C 124 | 30 | 96.8 | 110000 | 4  | AAI99682_05  | Continuation (6 of |       |    |      |     |   |          |                    |
| C 125 | 30 | 96.8 | 110000 | 4  | AAI99682_06  | Continuation (7 of |       |    |      |     |   |          |                    |
| C 126 | 30 | 96.8 | 110000 | 4  | AAI99685_05  | Continuation (6 of |       |    |      |     |   |          |                    |
| C 127 | 30 | 96.8 | 110000 | 4  | AAI99685_06  | Continuation (7 of |       |    |      |     |   |          |                    |
| 128   | 30 | 96.8 | 110000 | 10 | ABS56454_18  | Continuation (19 o |       |    |      |     |   |          |                    |
| C 129 | 30 | 96.8 | 127098 | 10 | ADL13649     | Adl13649 Osteoarth |       |    |      |     |   |          |                    |
| C 130 | 30 | 96.8 | 165199 | 6  | ABK83460     | Abk83460 Human cDN |       |    |      |     |   |          |                    |
| C 131 | 30 | 96.8 | 349980 | 3  | AAF21609     | Aaf21609 Neisseria |       |    |      |     |   |          |                    |
| C 132 | 30 | 96.8 | 349980 | 3  | AAF21608     | Aaf21608 Neisseria |       |    |      |     |   |          |                    |
| C 133 | 30 | 96.8 | 349980 | 13 | ADT05648     | Adt05648 Haemophil |       |    |      |     |   |          |                    |
| C 134 | 28 | 90.3 | 21     | 4  | AAH62656     | Aah62656 Synapota  |       |    |      |     |   |          |                    |
| C 135 | 28 | 90.3 | 27     | 14 | AEC08359     | Aec08359 A. fumiga |       |    |      |     |   |          |                    |
| C 136 | 28 | 90.3 | 29     | 2  | AAAT06487    | Aat06487 Primer fo |       |    |      |     |   |          |                    |
| 137   | 28 | 90.3 | 29     | 2  | AAH11017     | Aat11017 E. coli m |       |    |      |     |   |          |                    |
| 138   | 28 | 90.3 | 29     | 9  | ADB23088     | Adb23088 E. coli m |       |    |      |     |   |          |                    |
| C 139 | 28 | 90.3 | 47     | 3  | AAB66795     | Aaz66795 Human map |       |    |      |     |   |          |                    |
| C 140 | 28 | 90.3 | 100    | 8  | ACD70514     | Acd70514 E. coli k |       |    |      |     |   |          |                    |
| C 141 | 28 | 90.3 | 121    | 11 | ADZ42623     | Adz42623 Human gen |       |    |      |     |   |          |                    |
| 142   | 28 | 90.3 | 125    | 2  | AAQ68987     | Aaq68987 Human-410 |       |    |      |     |   |          |                    |
| 143   | 28 | 90.3 | 125    | 2  | AAI03611     | Aat03611 Protocadh |       |    |      |     |   |          |                    |
| C 144 | 28 | 90.3 | 207    | 4  | AAI24733     | Aai24733 Probe #14 |       |    |      |     |   |          |                    |
| C 145 | 28 | 90.3 | 207    | 4  | ABA70006     | Aba70006 Human foe |       |    |      |     |   |          |                    |
| C 146 | 28 | 90.3 | 207    | 4  | AAI50119     | Aai50119 Probe #15 |       |    |      |     |   |          |                    |
| C 147 | 28 | 90.3 | 207    | 4  | ABA36831     | Aba36831 Probe #18 |       |    |      |     |   |          |                    |
| C 148 | 28 | 90.3 | 207    | 4  | AAK44110     | Aak44110 Human bon |       |    |      |     |   |          |                    |
| C 149 | 28 | 90.3 | 207    | 4  | AAK18214     | Aak18214 Human bra |       |    |      |     |   |          |                    |

## ALIGNMENTS

## RESULT 1

ADY98104

ID ADY98104 standard; DNA; 18 BP.

XX

XX ADY98104;

XX

DT 16-JUN-2005 (first entry)

XX

DE TIM-1 allele 1 insertion sequence.

XX

asthma; chromosome 5; aniaethmatic; immune disorder; inflammation;  
respiratory disease; atopic dermatitis; dermatological;  
dermatological disease; allergic rhinitis; antiallergic;  
antiinflammatory; ear; nose; throat disease; graft rejection;  
autoimmune disease; vaccine; transgenic animal; transgene;  
T cell immunoglobulin domain and mucin domain 1; allergy; screening;  
diagnostic; immunosuppressive; TIM-1; antigen; ss.

Mus musculus.

Key Location/Qualifiers

CDS 1..18

/\*tag= a

/partial

/product= "TIM-1 allele 1 insertion sequence"

/note= "No stop codon"

WO2005027854-A2.

31-MAR-2005.

15-SEP-2004; 2004WO-US031036.

15-SEP-2003; 2003US-00663497.

(STRD ) UNIV LELAND STANFORD JUNIOR.  
(DAND ) DANA FARBEN CANCER INST INC.

Mcintire JJ, Dekruyff R, Umetsu DT, Freeman G;

WPI; 2005-262648/27.

P-PSDB; ADY98105.

Diagnosing individuals predisposition to immunological disorder, involves  
analyzing individual for presence of one or more T cell immunoglobulin  
domain and mucin domain 1 (TIM-1) polymorphisms.

Claim 4; Page 59; 100pp; English.

The invention relates to a method of diagnosing an individual's  
predisposition to an immunological disorder, which involves analyzing the  
individual for the presence of one or more T cell immunoglobulin domain  
and mucin domain 1 (TIM-1) polymorphisms, where the presence of the  
polymorphism is indicative of an individual's predisposition to develop  
the immunological disorder. Also described are methods for: (i) treating  
an immunological disorder in an individual, which involves administering  
to the individual an agent that binds to a TIM polypeptide; and (ii) for  
screening a compound for treatment of an immunological disorder, involves  
contacting a candidate agent with a TIM-1 polypeptide and detecting the  
ability of the agent to bind to the TIM-1 polypeptide or to modulate TIM-  
1 activity. The following are disclosed: TIM polypeptides and  
polynucleotides; antibodies to TIM polypeptide; and transgenic animal  
comprising the TIM polynucleotide. The diagnostic method further involves  
analyzing the individual for the presence of hepatitis A virus (HAV)  
seropositivity. In (ii), the agent is an attenuated or inactivated HAV.  
The agent competes with HAV for binding to TIM-1. The method comprises  
contacting a biological sample comprising protein with an antibody that  
specifically binds to an epitope having the amino acid sequence Met-Thr-

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 1, 2006, 10:31:51 ; Search time 3418 Seconds  
(without alignments)  
168.381 Million cell updates/sec

Title: US-10-663-497a-25\_COPY\_158\_163

Perfect score: 31

Sequence: 1 MTTVP 6

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h  
-USER=US10663497 @CGN 1.1 5548 @runat\_01082006\_083558\_1259 -NCPU=6 -ICPU=3  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vl.\*  
11: gb\_ov.\*  
12: gb\_hcg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score    | Query Length | ID       | Description   |
|------------|----------|--------------|----------|---------------|
| 1          | 31 100.0 | 411 7        | BV236381 | S234P6518     |
| 2          | 31 100.0 | 420 15       | AB101460 | Streptococcus |
| 3          | 31 100.0 | 441 4        | AY148667 | Saccharom     |

|    |    |       |        |    |            |                    |
|----|----|-------|--------|----|------------|--------------------|
| 4  | 31 | 100.0 | 447    | 15 | AY186969   | Trichloro          |
| 5  | 31 | 100.0 | 509    | 2  | AX194572   | Sequence           |
| 6  | 31 | 100.0 | 520    | 4  | AY144866   | Saccharom          |
| 7  | 31 | 100.0 | 591    | 7  | BV283028   | S232P6162          |
| 8  | 31 | 100.0 | 667    | 5  | AY448733   | Cercocabu          |
| 9  | 31 | 100.0 | 718    | 7  | BV663407   | S217P6008          |
| 10 | 31 | 100.0 | 863    | 7  | BV032503   | S212P6885          |
| 11 | 31 | 100.0 | 906    | 2  | AR484494   | Sequence           |
| 12 | 31 | 100.0 | 906    | 2  | AX143103   | Sequence           |
| 13 | 31 | 100.0 | 948    | 8  | DQ331823   | Synthetic          |
| 14 | 31 | 100.0 | 950    | 7  | BV479132   | td112c10.          |
| 15 | 31 | 100.0 | 951    | 4  | AY144967   | Saccharom          |
| 16 | 31 | 100.0 | 954    | 6  | BC099515   | Mus muscu          |
| 17 | 31 | 100.0 | 1026   | 7  | CNS061PY   | T3 end of          |
| 18 | 31 | 100.0 | 1041   | 7  | CNS06F13   | T7 end of          |
| 19 | 31 | 100.0 | 1059   | 2  | AX507393   | Sequence           |
| 20 | 31 | 100.0 | 1059   | 2  | AX651611   | Sequence           |
| 21 | 31 | 100.0 | 1104   | 2  | AR550575   | Sequence           |
| 22 | 31 | 100.0 | 1243   | 6  | BC058428   | Mus muscu          |
| 23 | 31 | 100.0 | 1274   | 2  | AR627172   | Sequence           |
| 24 | 31 | 100.0 | 1319   | 2  | AR575922   | Sequence           |
| 25 | 31 | 100.0 | 1319   | 4  | AF061638   | Arabidops          |
| 26 | 31 | 100.0 | 1448   | 2  | AX072920   | Sequence           |
| 27 | 31 | 100.0 | 2194   | 4  | SCU46559   | Saccharomyc        |
| 28 | 31 | 100.0 | 3020   | 4  | SCYNR034W  | Z71649 S.cerevisia |
| 29 | 31 | 100.0 | 3112   | 2  | BD158192   | Primer fo          |
| 30 | 31 | 100.0 | 3112   | 2  | AX880097   | Sequence           |
| 31 | 31 | 100.0 | 3112   | 5  | AK023070   | Homo sapi          |
| 32 | 31 | 100.0 | 3259   | 2  | AX486044   | Sequence           |
| 33 | 31 | 100.0 | 3259   | 2  | AX145408   | Sequence           |
| 34 | 31 | 100.0 | 3259   | 15 | AF270090   | Staphyloc          |
| 35 | 31 | 100.0 | 3349   | 2  | AR485421   | Sequence           |
| 36 | 31 | 100.0 | 3349   | 2  | AX144785   | Sequence           |
| 37 | 31 | 100.0 | 3349   | 15 | AF269465   | Staphyloc          |
| 38 | 31 | 100.0 | 3703   | 15 | DQ028634   | Mycobacte          |
| 39 | 31 | 100.0 | 3713   | 2  | AR485694   | Sequence           |
| 40 | 31 | 100.0 | 3713   | 2  | AX145058   | Sequence           |
| 41 | 31 | 100.0 | 3713   | 15 | AF269740   | Staphyloc          |
| 42 | 31 | 100.0 | 3840   | 4  | YSCPAMIBEN | Yeast para-        |
| 43 | 31 | 100.0 | 4259   | 4  | SCU43608   | Saccharomyc        |
| 44 | 31 | 100.0 | 9389   | 15 | ST250581   | Streptomy          |
| 45 | 31 | 100.0 | 11382  | 2  | AR619509   | Sequence           |
| 46 | 31 | 100.0 | 11425  | 15 | AE009708   | Brucella           |
| 47 | 31 | 100.0 | 13380  | 5  | HSV11740   | H.sapiens w        |
| 48 | 31 | 100.0 | 13759  | 15 | AE005041   | Halobacte          |
| 49 | 31 | 100.0 | 26276  | 13 | U88177     | Caenorhabd1        |
| 50 | 31 | 100.0 | 37500  | 2  | CQ767413   | Sequence           |
| 51 | 31 | 100.0 | 37500  | 2  | CQ774651   | Sequence           |
| 52 | 31 | 100.0 | 43158  | 12 | CR933778   | Danio rer          |
| 53 | 31 | 100.0 | 49295  | 11 | BX571669   | Zebrafish          |
| 54 | 31 | 100.0 | 53951  | 5  | AC092866   | Homo sapi          |
| 55 | 31 | 100.0 | 56963  | 12 | CR974590_3 | Continuation (4 of |
| 56 | 31 | 100.0 | 61744  | 12 | AL713961   | Danio rer          |
| 57 | 31 | 100.0 | 61817  | 11 | AL749527   | Zebrafish          |
| 58 | 31 | 100.0 | 62246  | 12 | AC180220   | Strongylo          |
| 59 | 31 | 100.0 | 63649  | 1  | AY576273   | Bacterioph         |
| 60 | 31 | 100.0 | 69614  | 12 | AC083925   | Homo sapi          |
| 61 | 31 | 100.0 | 71506  | 5  | AC092452   | Homo sapi          |
| 62 | 31 | 100.0 | 73431  | 12 | AP000575   | Homo sapi          |
| 63 | 31 | 100.0 | 84208  | 12 | AP008109   | Lotus cor          |
| 64 | 31 | 100.0 | 84388  | 5  | AL589984   | Human DNA          |
| 65 | 31 | 100.0 | 85975  | 5  | AC110011   | Homo sapi          |
| 66 | 31 | 100.0 | 87230  | 12 | AP007492   | Lotus cor          |
| 67 | 31 | 100.0 | 87967  | 4  | AC005223   | Arabidops          |
| 68 | 31 | 100.0 | 88917  | 11 | AL929169   | Zebrafish          |
| 69 | 31 | 100.0 | 92112  | 2  | CQ893967   | Sequence           |
| 70 | 31 | 100.0 | 95356  | 5  | AL139112   | Human DNA          |
| 71 | 31 | 100.0 | 96217  | 5  | AL645729   | Human DNA          |
| 72 | 31 | 100.0 | 96579  | 11 | CR848001   | Zebrafish          |
| 73 | 31 | 100.0 | 97512  | 5  | AL139351   | Human DNA          |
| 74 | 31 | 100.0 | 98461  | 4  | ATT6H20    | Arabidops          |
| 75 | 31 | 100.0 | 103979 | 12 | AC167040   | Bos tauru          |
| 76 | 31 | 100.0 | 104423 | 12 | AP008156   | Lotus cor          |

|     |    |       |        |    |              |                     |
|-----|----|-------|--------|----|--------------|---------------------|
| 77  | 31 | 100.0 | 105075 | 12 | CT573793     | CT573793 Danio rer  |
| 78  | 31 | 100.0 | 106886 | 5  | AP001462     | AP001462 Homo sapi  |
| 79  | 31 | 100.0 | 107415 | 5  | AL513365     | AL513365 Human DNA  |
| 80  | 31 | 100.0 | 107480 | 5  | AC073118     | AC073118 Homo sapi  |
| 81  | 31 | 100.0 | 107965 | 5  | AC093678     | AC093678 Homo sapi  |
| 82  | 31 | 100.0 | 109290 | 12 | HS838114     | Y12335 Homo sapien  |
| 83  | 31 | 100.0 | 110000 | 4  | AP008212_050 | Continuation (51 o  |
| 84  | 31 | 100.0 | 110000 | 4  | AP008212_207 | Continuation (208   |
| 85  | 31 | 100.0 | 110000 | 4  | AP008213_149 | Continuation (150   |
| 86  | 31 | 100.0 | 110000 | 4  | AP008216_217 | Continuation (218   |
| 87  | 31 | 100.0 | 110000 | 4  | CR380959_10  | Continuation (11 o  |
| 88  | 31 | 100.0 | 110000 | 4  | CR382123_07  | Continuation (8 of  |
| 89  | 31 | 100.0 | 110000 | 4  | CR382132_38  | Continuation (39 o  |
| 90  | 31 | 100.0 | 110000 | 4  | CR382135_11  | Continuation (12 o  |
| 91  | 31 | 100.0 | 110000 | 4  | AE016818_11  | Continuation (12 o  |
| 92  | 31 | 100.0 | 110000 | 4  | AE016959_217 | Continuation (218 o |
| 93  | 31 | 100.0 | 110000 | 4  | AE017343_17  | Continuation (18 o  |
| 94  | 31 | 100.0 | 110000 | 4  | AE017345_09  | Continuation (10 o  |
| 95  | 31 | 100.0 | 110000 | 4  | AP007150_14  | Continuation (15 o  |
| 96  | 31 | 100.0 | 110000 | 4  | AP007157_08  | Continuation (9 of  |
| 97  | 31 | 100.0 | 110000 | 4  | AP008207_216 | Continuation (172   |
| 98  | 31 | 100.0 | 110000 | 4  | AP008209_171 | Continuation (172   |
| 99  | 31 | 100.0 | 110000 | 12 | AC140527_2   | Continuation (3 of  |
| 100 | 31 | 100.0 | 110000 | 12 | AP006502_09  | Continuation (10 o  |
| 101 | 31 | 100.0 | 110000 | 12 | EX901880_0   | EX901880 Danio rer  |
| 102 | 31 | 100.0 | 110000 | 12 | CR974590_2   | Continuation (3 of  |
| 103 | 31 | 100.0 | 110000 | 12 | TANN1_09     | Continuation (10 o  |
| 104 | 31 | 100.0 | 110000 | 12 | TANN3_06     | Continuation (7 of  |
| 105 | 31 | 100.0 | 110000 | 12 | TANN3_07     | Continuation (8 of  |
| 106 | 31 | 100.0 | 110000 | 15 | CP000089_17  | Continuation (18 o  |
| 107 | 31 | 100.0 | 110000 | 15 | CP000094_08  | Continuation (9 of  |
| 108 | 31 | 100.0 | 110000 | 15 | CP000097_15  | Continuation (16 o  |
| 109 | 31 | 100.0 | 110000 | 15 | CP000110_05  | Continuation (6 of  |
| 110 | 31 | 100.0 | 110000 | 15 | CP000112_15  | Continuation (16 o  |
| 111 | 31 | 100.0 | 110000 | 15 | CP000143_00  | CP000143 Rhodobact  |
| 112 | 31 | 100.0 | 110000 | 15 | CP000155_12  | Continuation (13 o  |
| 113 | 31 | 100.0 | 110000 | 15 | CR543861_13  | Continuation (14 o  |
| 114 | 31 | 100.0 | 110000 | 15 | U00089_4     | Continuation (5 of  |
| 115 | 31 | 100.0 | 110000 | 15 | AE014292_05  | Continuation (6 of  |
| 116 | 31 | 100.0 | 110000 | 15 | AE015929_14  | Continuation (15 o  |
| 117 | 31 | 100.0 | 110000 | 15 | AE015928_22  | Continuation (23 o  |
| 118 | 31 | 100.0 | 110000 | 15 | AE016825_44  | Continuation (45 o  |
| 119 | 31 | 100.0 | 110000 | 15 | AE016825_45  | Continuation (46 o  |
| 120 | 31 | 100.0 | 110000 | 15 | AE017224_06  | Continuation (7 of  |
| 121 | 31 | 100.0 | 110000 | 15 | AE017285_06  | Continuation (7 of  |
| 122 | 31 | 100.0 | 110000 | 15 | AM040265_06  | Continuation (7 of  |
| 123 | 31 | 100.0 | 110000 | 15 | AP006618_49  | Continuation (50 o  |
| 124 | 31 | 100.0 | 110000 | 15 | AP006840_06  | Continuation (7 of  |
| 125 | 31 | 100.0 | 110000 | 15 | AY596297_22  | Continuation (23 o  |
| 126 | 31 | 100.0 | 110000 | 15 | BA000002_15  | Continuation (16 o  |
| 127 | 31 | 100.0 | 110000 | 15 | BA000012_58  | Continuation (59 o  |
| 128 | 31 | 100.0 | 110000 | 15 | BA000013_64  | Continuation (65 o  |
| 129 | 31 | 100.0 | 110000 | 15 | BA000030_68  | Continuation (69 o  |
| 130 | 31 | 100.0 | 110000 | 15 | CP000029_13  | Continuation (14 o  |
| 131 | 31 | 100.0 | 110000 | 12 | CP000029_22  | Continuation (23 o  |
| 132 | 31 | 100.0 | 110334 | 12 | AC170219     | AC170219 Bos tauru  |
| 133 | 31 | 100.0 | 113053 | 12 | AC108087     | AC108087 Homo sapi  |
| 134 | 31 | 100.0 | 115224 | 5  | AL359539     | AL359539 Human DNA  |
| 135 | 31 | 100.0 | 119796 | 6  | AL663079     | AL663079 Mouse DNA  |
| 136 | 31 | 100.0 | 121598 | 11 | CR847844     | CR847844 Zebrafish  |
| 137 | 31 | 100.0 | 121913 | 14 | AC170740     | AC170740 Sorex ara  |
| 138 | 31 | 100.0 | 122379 | 5  | AL359715     | AL359715 Human DNA  |
| 139 | 31 | 100.0 | 122449 | 4  | AP006666     | AP006666 Lotus cor  |
| 140 | 31 | 100.0 | 123219 | 2  | AX195073     | AX195073 Sequence   |
| 141 | 31 | 100.0 | 123794 | 5  | AC015917     | AC015917 Homo sapi  |
| 142 | 31 | 100.0 | 127219 | 12 | AC023806     | AC023806 Mus muscu  |
| 143 | 31 | 100.0 | 127393 | 12 | AC119051     | AC119051 Gallus ga  |
| 144 | 31 | 100.0 | 127973 | 12 | AC158279     | AC158279 Spherooid  |
| 145 | 31 | 100.0 | 130748 | 12 | AP005906     | AP005906 Oryza sat  |
| 146 | 31 | 100.0 | 130984 | 12 | AC022766     | AC022766 Homo sapi  |
| 147 | 31 | 100.0 | 135001 | 12 | AC150111     | AC150111 Gallus ga  |
| 148 | 31 | 100.0 | 135634 | 12 | AP005253     | AP005253 Oryza sat  |
| 149 | 31 | 100.0 | 135983 | 12 | AC134767     | AC134767 Rattus no  |

|     |    |       |        |    |          |                    |
|-----|----|-------|--------|----|----------|--------------------|
| 150 | 31 | 100.0 | 137259 | 12 | AC010392 | AC010392 Homo sapi |
|-----|----|-------|--------|----|----------|--------------------|

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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GenCore version 5.1.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 4, 2006, 19:20:46 ; Search time 102 Seconds  
(without alignments)  
139.750 Million cell updates/sec

Title: US-10-663-497A-25\_COPY\_158\_163  
Perfect score: 31  
Sequence: 1 MTTTVP 6

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-O=/abss/ABSSEB\_spool/US1063497/runat\_01082006\_083608\_1450/app\_query.fasta 1  
-NA=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LODPL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cgi -LIST=150 -DOCALLGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abs804  
-USER=US1063497@CGN\_1\_91 @runat\_01082006\_083608\_1450 -NCPU=6 -ICPU=3  
-NO MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:

1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                      | Description       |
|------------|-------|-------------|--------|-------------------------|-------------------|
| 1          | 31    | 100.0       | 25     | 7 US-11-348-413-436439  | Sequence 436439,  |
| 2          | 31    | 100.0       | 25     | 7 US-11-348-413-436440  | Sequence 436440,  |
| 3          | 31    | 100.0       | 25     | 7 US-11-348-413-496650  | Sequence 496650,  |
| 4          | 31    | 100.0       | 25     | 7 US-11-348-413-496651  | Sequence 496651,  |
| c 5        | 31    | 100.0       | 25     | 7 US-11-348-413-531853  | Sequence 531853,  |
| c 6        | 31    | 100.0       | 25     | 7 US-11-348-413-531854  | Sequence 531854,  |
| 7          | 31    | 100.0       | 25     | 7 US-11-348-413-1077807 | Sequence 1077807, |
| 8          | 31    | 100.0       | 25     | 7 US-11-348-413-1143851 | Sequence 1143851, |

|       |        |   |                       |                    |
|-------|--------|---|-----------------------|--------------------|
| 100.0 | 25     | 7 | US-11-348-413-1143852 | Sequence 1143852,  |
| 100.0 | 25     | 7 | US-11-348-413-1143853 | Sequence 1143853,  |
| 100.0 | 25     | 7 | US-11-348-413-1143854 | Sequence 1143854,  |
| 100.0 | 25     | 7 | US-11-348-413-1143855 | Sequence 1143855,  |
| 100.0 | 25     | 7 | US-11-348-413-1143856 | Sequence 1143856,  |
| 100.0 | 25     | 7 | US-11-348-413-1143857 | Sequence 1143857,  |
| 100.0 | 25     | 7 | US-11-348-413-1143858 | Sequence 1143858,  |
| 100.0 | 25     | 7 | US-11-348-413-1189177 | Sequence 1189177,  |
| 100.0 | 25     | 7 | US-11-348-413-1189178 | Sequence 1189178,  |
| 100.0 | 25     | 7 | US-11-348-413-1189179 | Sequence 1189179,  |
| 100.0 | 25     | 7 | US-11-348-413-1189180 | Sequence 1189180,  |
| 100.0 | 25     | 7 | US-11-348-413-1189181 | Sequence 1189181,  |
| 100.0 | 25     | 7 | US-11-348-413-1189182 | Sequence 1189182,  |
| 100.0 | 25     | 7 | US-11-348-413-1189183 | Sequence 1189183,  |
| 100.0 | 25     | 7 | US-11-348-413-1189184 | Sequence 1189184,  |
| 100.0 | 122    | 7 | US-11-348-413-14913   | Sequence 14913, A  |
| 100.0 | 122    | 7 | US-11-348-413-16206   | Sequence 16206, A  |
| 100.0 | 533    | 8 | US-11-266-748A-426895 | Sequence 426895,   |
| 100.0 | 906    | 7 | US-11-348-413-13150   | Sequence 13150, A  |
| 100.0 | 948    | 8 | US-11-217-529-75768   | Sequence 75768, A  |
| 100.0 | 966    | 8 | US-11-217-529-78409   | Sequence 78409, A  |
| 100.0 | 969    | 8 | US-11-217-529-2252    | Sequence 2252, Ap  |
| 100.0 | 1000   | 8 | US-11-266-748A-398903 | Sequence 398903,   |
| 100.0 | 1000   | 8 | US-11-266-748A-469949 | Sequence 469949,   |
| 100.0 | 1338   | 7 | US-11-174-307B-2539   | Sequence 2539, Ap  |
| 100.0 | 1338   | 7 | US-11-056-355B-103384 | Sequence 103384,   |
| 100.0 | 1338   | 7 | US-11-056-355B-114623 | Sequence 114623,   |
| 100.0 | 1339   | 7 | US-11-174-307B-427    | Sequence 427, App  |
| 100.0 | 1339   | 7 | US-11-056-355B-35111  | Sequence 35111, A  |
| 100.0 | 1432   | 7 | US-11-174-307B-1099   | Sequence 1099, Ap  |
| 100.0 | 1432   | 7 | US-11-056-355B-7474   | Sequence 7474, Ap  |
| 100.0 | 3112   | 8 | US-11-266-748A-29930  | Sequence 29930, A  |
| 100.0 | 5988   | 8 | US-11-217-529-505     | Sequence 505, App  |
| 100.0 | 138627 | 6 | US-10-540-898-159     | Sequence 159, App  |
| 100.0 | 151830 | 6 | US-10-519-335-37      | Sequence 37, Appl  |
| 96.8  | 651    | 6 | US-10-374-780A-1340   | Sequence 1340, Ap  |
| 96.8  | 4306   | 6 | US-10-473-173-72      | Sequence 72, Appl  |
| 96.8  | 4877   | 8 | US-11-266-748A-29220  | Sequence 29220, A  |
| 90.3  | 25     | 8 | US-11-217-529-134239  | Sequence 134239,   |
| 90.3  | 393    | 8 | US-11-266-748A-169632 | Sequence 169632,   |
| 90.3  | 393    | 8 | US-11-266-748A-299752 | Sequence 299752,   |
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; Publication No. US20060160121A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; APPLICANT: Murphy, Ellen  
; APPLICANT: Olmsted, Stephen  
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
; FILE REFERENCE: 031896-084100 (AM 101724)  
; CURRENT APPLICATION NUMBER: US/11/348,413  
; CURRENT FILING DATE: 2006-02-07  
; PRIOR APPLICATION NUMBER: PCT/US05/035471  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US 11/243,445  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US 60/615,573  
; PRIOR FILING DATE: 2004-10-05  
; NUMBER OF SEQ ID NOS: 1276209  
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; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; APPLICANT: Murphy, Ellen  
; APPLICANT: Olmsted, Stephen  
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
; FILE REFERENCE: 031896-084100 (AM 101724)  
; CURRENT APPLICATION NUMBER: US/11/348,413  
; CURRENT FILING DATE: 2006-02-07  
; PRIOR APPLICATION NUMBER: PCT/US05/035471  
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; PRIOR APPLICATION NUMBER: US 11/243,445  
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; PRIOR APPLICATION NUMBER: US 60/615,573  
; PRIOR FILING DATE: 2004-10-05  
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; LENGTH: 25  
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; FEATURE:  
; OTHER INFORMATION: probe

## ALIGNMENTS



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| ; Sequence 697602, Application US/10310914A                         |    |      |         |    |                       |                    |
| ; Publication No. US2006000322A1                                    |    |      |         |    |                       |                    |
| ; GENERAL INFORMATION:  |    |      |         |    |                       |                    |
| ; APPLICANT: Bentwich, Isaac  |    |      |         |    |                       |                    |
| ; APPLICANT: Shiler, Kruzat   |    |      |         |    |                       |                    |
| ; TITLE OF INVENTION: Bioinformatically detectable group of novel   |    |      |         |    |                       |                    |
| ; TITLE OF INVENTION: uses thereof                                  |    |      |         |    |                       |                    |
| ; FILE REFERENCE: 06087.0200.CPUS01                                 |    |      |         |    |                       |                    |
| ; CURRENT APPLICATION NUMBER: US/10/310,914A                        |    |      |         |    |                       |                    |
| ; CURRENT FILING DATE: 2002-12-06                                   |    |      |         |    |                       |                    |
| ; NUMBER OF SEQ ID NOS: 1388402                                     |    |      |         |    |                       |                    |
| ; SOFTWARE: PatentIn version 3.3                                    |    |      |         |    |                       |                    |
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| ; Sequence 14597, Application US/10215112                           |    |      |         |    |                       |                    |
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| ; GENERAL INFORMATION:  |    |      |         |    |                       |                    |
| ; APPLICANT: Michael Mittmann                                       |    |      |         |    |                       |                    |
| ; TITLE OF INVENTION: Method of Genetic Analysis of Probes:         |    |      |         |    |                       |                    |
| ; FILE REFERENCE: Test3   |    |      |         |    |                       |                    |
| ; CURRENT APPLICATION NUMBER: US/10/215,112                         |    |      |         |    |                       |                    |
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| ; OTHER INFORMATION: Synthetic Oligonucleotide                      |    |      |         |    |                       |                    |
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| Score: 31.00 Matches: 6   |    |      |         |    |                       |                    |
| Percent Similarity: 100.0% Conservative: 0                          |    |      |         |    |                       |                    |
| Best Local Similarity: 100.0% Mismatches: 0                         |    |      |         |    |                       |                    |
| Query Match: 100.0% Indels: 0                                       |    |      |         |    |                       |                    |
| DB: 6 Gaps: 0   |    |      |         |    |                       |                    |
| US-10-663-497A-25_COPY_158_163 (1-6) x US-10-215-112-14597 (1-25)   |    |      |         |    |                       |                    |
| QY 1 MetThrThrThrValPro 6   |    |      |         |    |                       |                    |